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Identification of favourable alleles in the parents for the improvement of superior hybrids in cotton (*Gossypium hirsutum* L.).

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ABSTRACT

Forty five Cotton hybrids along with their parents were studied in three different locations (Regional Agricultural Research Station, Lam, Guntur, Agricultural Research Station, Jangamaheswarapuram and Agricultural Research Station, Darsi) in Andhra Praesh. The data on differeent parameters like seed cotton yield (g/plant), 2.5% span length (mm), lint index (g) and boll weight (g) were recorded in each location and were averaged and were used for calculating the different parameters of the model. Identification of unique favourable alleles in the donor parents analysis revealed that for improving NDLH 1938 × RAH 1004 hybrid for 2.5 % span length, the donor parent SURABHI and for lint index L 788 and NA 1325 were showed significant positive μG' estimates. Whereas, for boll weight, three parents, viz L 788, L 770 and L 604, showed the significant positive μG' estimates in combined analysis. Only one parent i.e., G COT 16, showed the significant positive μG' estimates in combined analysis for boll weight for improving NDLH 1938 × L 770 hybrid.

Keywords: *Cotton, favourable allleles*

India is playing a predominant role in the global cotton scenario due to several distinct features such as largest cotton growing area, cultivation of all the four cultivated species. The crop improvement programme primarily lay emphasis on the development of hybrids particularly for the yield by several recycling procedures and considerable success also has been obtained. The resulting improvement obtained in the hybrid due to accumulation of higher frequency of favourable alleles coming from the recycled parents, represented the net improvement in hybrid performance after accounting for the number of favourable alleles lost during selection. Dudley (1984a) first proposed a methodology for identification of unique favourable alleles in donor inbred lines of maize for improving the parental constituents in a desirable single cross. His first method was followed by several modifications by him as well as by other workers (Dudley, 1987b, Zanoni and Dubley, 1989b and Bernardo, 1990) devising new parameters for evaluating the donor inbred lines from all aspects like frequency of favourable alleles present, frequency of alleles lacking in the parents, estimating the relative relationships of the donor inbred and also estimating the loss of alleles not only in the donor parents but also in the single cross hybrids of maize. Based on the experiences of the several workers i.e., Dudley (1987a), Zanoni and Dudley (1989a), Zanoni and Dudley (1989b), Reddy *et al*. (2003), Reddy *et al*. (2004), Reddy *et al*. (2005) and Saida Naik (2012) in the maize crop an attempt was made in the present experiment for identification of favourable alleles in the donor parents in cotton. The identification of favourable alleles in parental lines is a fundamental strategy for developing superior hybrids in upland cotton (*Gossypium hirsutum* L.). This process shifts the focus from simple physical observation to understanding the precise genetic drivers of "hybrid vigour" (heterosis) particularly core importance in hybrid improvement like predicting hybrid performance, maximizing heterosis, targeted trait enhancement and Strategic Breeding applications like parental improvement, molecular design breeding and breaking negative correlations.

MATERIAL AND METHODS

A set of ten parents *viz.,* NDLH 1938, L 788, L 770, NA 1325, L604, SURABHI, RAH 1004, HYPS 152, MCU 5 and G COT 16 were selected based on their performance in genetic

divergence study carried out with 63 genotypes during *kharif*, 2012-13 and forty five intra-specific cross combinations were made in diallel fashion without reciprocals during off season (2013) at RARS Lam Farm, Guntur, Andhra Pradesh. The evaluation of hybrids along with parents was done at three locations i.e., Regional Agricultural Research Station (RARS) Lam Farm, Agricultural Research Station (ARS), Jangamaheswarapuram (J M Puram) and Agricultural Research Station (ARS), Darsi during *kharif*, 2013-14. In each location, experimental plot consisted of three rows of 6m length with a row to row spacing of 120cm and plant to plant distance of 60cm. The data on differeent parameters like seed cotton yield (g/ plant), 2.5% span length (mm), lint index (g) and boll weight (g) were recorded in each location and the averages were used for calculating the different parameters of the model. The identification of favouarble alleles for the above characters present in the donor plant (from now onwards designated as ìG') but not in the hybrid to be improved was carried out by using Dudley [2] model. Besides ìG,' other parameters of the model mB', mC', mD', mE' and mF' were also calculated.

RESULTS AND DISCUSSION

The estimates ìG' in the eight parental lines for four traits have been presented for combined analysis for each cross in Tables 1 to 6.

NDLH 1938 × L 604

Out of all the hybrids, the hybrid NDLH 1938 × L 604 was designated as the first superior hybrid to be improved based on the mean, *per se* performance in all the locations and presumed that further scope of improvement by other means.

The estimates of ìG' in the eight donor parents and the cross NDLH 1938 × L 604 for the four traits were reported in Table 1.

For all the characters (seed cotton yield plant^{-1}, 2.5 % span length, lint index and boll weight) studied in combined analysis, all the eight parents had non significant ìG' estimates. It is observed that the donor parents L 770 and RAH 1004 eventhough showed non significant positive ìG' estimates for the seed cotton yield, the ìG' estimates were high indicating existence of favourable alleles for further improvement of the target hybrid.

Table 1. Estimates of μG' in the donor parents for important quantitative and qualitative traits combined over environments, when the hybrid NDLH 1938 × L 604 (first superior cross) was designated as the hybrid to be improved

Parent	μG'			
	Seed cotton yield plant^{-1} (g)	2.5% span length (mm)	Lint index (g)	Boll weight (g)
L 788	3.875 [b]	- 0.655 [b]	N	0.030 [b]
L 770	5.817 [b]	0.037 [a]	0.050 [a]	0.053 [b]
NA 1325	- 4.993 [b]	- 1.157 [a]	N	- 0.155 [b]
SURABHI	1.767 [b]	- 0.183 [a]	- 0.095 [a]	0.018 [b]
RAH 1004	6.480 [b]	- 2.060 [b]	N	- 0.005 [b]
HYPS 152	0.932 [b]	- 0.173 [a]	N	- 0.062 [b]
MCU 5	- 9.363 [b]	- 0.308 [a]	N	- 0.180 [a]
G COT 16	- 9.830 [b]	- 0.003 [a]	N	- 0.175 [b]
SE a	-	0.494	0.061	0.071
SE b	5.337	0.403		0.071
SE c	-	-	-	-
SE d	-	-	-	-

* Larger than 2 x SE; N = μG' values could not obtained

a = q_{j0}, q_{kl} b = q_{j1}, q_{k0} c = q_{j0}, q_{j1} d = q_{k0}, q_{k1}

However, for further characterization of various donor parents and their genetic similarity estimates (Table 2) the information on other estimates (mB' to mG') have to be analyzed to initiate the breeding programme for this cross. Hence, as reasons mentioned earlier, the genetic enhancement for boll weight is only considered.

In order to obtain further details about the nature and frequency of alleles in the donor parents *vis-a-vis* concerned superior cross, the various parameters to represent the different classes and the relationship of the donor parents with the parents of the cross concerned are presented in Table 2. It could be concluded from this table that L 788, L 770 and RAH 1004 were the donor parents possessing high frequency of positive alleles mG' are not present in the constituents of the hybrid. Even though these parents having positive alleles, the resulting hybrid with the combination of these parents with parents of superior cross had lower boll weight indicating that these parents are not suitable for the improvement of this superior cross. The reasons may be attributed to the higher mD' and mF' values than the mG'.

NDLH 1938 × RAH 1004

The estimate of ìG' in the donor parents, when the hybrid to be improved is NDLH 1938 × RAH 1004, are presented in Table 3.

For seed cotton yield plant^{-1} all the donor parents showed non significant ìG' estimates. However, for 2.5 % span length, SURABHI and for lint index L 788 and NA 1325 showed the significant positive ìG' estimates. Where as for boll weight, three parents *viz*., L 788, L 770 and L 604 showed the significant positive ìG' estimates in combined analysis.

However, further characterization of various donor parents and their genetic similarity estimates (Table 4) have to be considered along with the other estimates (mB' to mG') to initiate the improvement programme for this cross. For this cross also, as mentioned earlier, the genetic enhancement for boll weight is only considered.

The cross, NDLH 1938 × RAH 1004, had the better mean *per se* value out of 45 crosses originating from 10 × 10 half diallel. It was observed that out of eight donors namely, L 788, L 770 and L 604 gave significant positive mG' values. Critical study of mean *per se* value of the crosses and different parameters of the model taken into consideration together (Table 4) indicated that the donor parents L 770 and L 604 showed the highest significant mG' estimate (0.290) and the donors also gave higher mean value in its cross combinations with the NDLH 1938. However, it is interesting to note that the same donors when crossed with RAH 1004 gave the values lower than the NDLH 1938 × RAH 1004 which could be

Table 2. Estimates of µB' …… µG' for boll weight in eight donor parents when NDLH 1938 × L 604 is the hybrid to be improved

	Class of loci										
Parents	**µB'**	**µC'**	**µD'**	**µE'**	**µF'**	**µG'**	**µC+F'**	**µD+E'**	**Genetic affinity with**	**Mean *per se* of NDLH 1938 x donor**	**Mean *per se* of L 604 x donor**
L 788	-0.14	0.260*	0.290*	0.01	0.260*	0.03	0.520*	0.300*	L 604	4.28	4.22
L 770	-0.02	0.102	0.447*	0.168	0.102	0.053	0.205*	0.615*	L 604	4.64	3.95
NA 1325	-0.01	0.420*	0.13	0.13	0.14	-0.16	0.560*	0.260*	NDLH 1938	4.15	4.17
SURABHI	-0.13	0.127	0.422*	0.143	0.127	0.018	0.255*	0.565*	L 604	4.52	3.93
RAH 1004	0.085	0.245*	0.305*	0.025	0.245*	-0.01	0.490*	0.330*	L 604	4.24	4.12
HYPS 152	0.158	0.417*	0.133	0.133	0.137	-0.06	0.555*	0.265*	NDLH 1938	4.34	4.35
MCU 5	-0.04	0.445*	0.105	0.105	0.165	-0.18	0.610*	0.210*	NDLH 1938	4.05	4.17
G COT 16	-0.31	0.065	0.485*	0.205*	0.065	-0.18	0.13	0.690*	L 604	4.26	3.43

@ Mean *per se* of the cross NDLH 1938 × L 604 is: 4.74

* Larger than 2 x S.E. a= q_{jo}, q_{k1}; b= q_{j1}, q_{ko}; c= q_{jo}, q_{j1}; d= q_{ko}, q_{k1}

Table 3. Estimates of mG' in the donor parents for important quantitative and qualitative traits combined over environments, when the hybrid NDLH 1938 × RAH 1004 (second superior cross) was designated as the hybrid to be improved

Parent	μG'			
	Seed cotton yield plant^{-1} (g)	2.5% span length (mm)	Lint index (g)	Boll weight (g)
L 788	1.112 [b]	N	0.267*[a]	0.155* [b]
L 770	8.342 [b]	N	- 0.088 [a]	0.290* [b]
NA 1325	- 2.488 [b]	N	0.148* [a]	0.123 [b]
L 604	6.428 [b]	N	N	0.290* [b]
SURABHI	- 2.025 [b]	1.255* [b]	N	N
HYPS 152	- 3.358 [b]	N	- 0.493 [a]	0.098 [b]
MCU 5	- 15.085 [a]	N	N	- 0.082 [a]
G COT 16	- 3.990 [b]	N	N	0.120 [b]
SE a	5.337	-	0.061	0.071
SE b	5.337	0.403		0.071
SE c	-	-	-	-
SE d	-	-	-	-

* Larger than 2 x SE; N = μG' values could not obtained

a = q_{j0}, q_{kl} b = q_{j1}, q_{k0} c = q_{j0}, q_{j1} d = q_{k0}, q_{k1}

Table 4. Estimates of μB' …… μG' for boll weight in eight donor parents when NDLH 1938 × RAH 1004 is the hybrid to be improved

	Class of loci										
Parents	μB'	μC'	μD'	μE'	μF'	μG'	μC+F'	μD+E'	Genetic affinity with	Mean *per se* of NDLH 1938 x donor	Mean *per se* o RAH 1004 x donor
L 788	-0.105	0.135	0.255*	-0.12	0.135	0.155*	0.270*	0.14	RAH 1004	4.28	4.04
L 770	0.13	0.09	0.300*	-0.07	0.09	0.290*	0.18	0.230*	RAH 1004	4.64	4.22
NA 1325	-0.097	0.167*	0.222*	-0.15	0.167*	0.123	0.335*	0.075	RAH 1004	4.15	4.03
L 604	0.200*	0.04	0.350*	-0.02	0.04	0.290*	0.08	0.330*	RAH 1004	4.74	4.12
SURABHI	N	N	N	N	N	N	N	N	N	4.24	4.12
HYPS 152	-0.052	0.047	0.342*	-0.03	0.047	0.098	0.095	0.315*	RAH 1004	4.34	3.75
MCU 5	0.062	0.382*	0.008	0.008	0.012	-0.082	0.395*	0.015	NDLH	4.05	4.06
G COT 16	-0.105	0.11	0.280*	-0.09	0.11	0.12	0.220*	0.19	RAH 1004	4.26	3.92

attributed to differences in the mD' (the class in which P2 and Pw have unfavourable alleles and P1 has favourable alleles) values. Hence, the favourable alleles contributed by L 604 and L 770 (0.290) were nullified by the favourable alleles lost due to substitution of NDLH 1938 (mD'=0.350 for L 604 and 0.300 for L 770).

If enhancement is sought through the improvement of parents, the donors L 770 and L 604 may be suggested to improve NDLH 1938, as these donors have higher mG' values compared to the rest. Considering the parameters (mD'+mE'), it was found that the parent NDLH 1938 had greater affinity with these donors. Hence, the parent NDLH 1938 can be

utilized for the improvement through pedigree breeding by crossing to L 770 and L 604.

NDLH 1938 × L 770

The estimates of ìG' in the donor lines, when the hybrid to be improved is NDLH 1938 × L 770 are presented in Table 5.

For seed cotton yield plant^{-1}, 2.5 % span length and lint index all the donor parents showed non significant ìG' estimates. Where as for boll weight only one parent G COT 16 showed significant positive ìG' estimates in combined analysis.

It is observed that the donor parents, L 770 and RAH 1004, eventhough showed non significant positive ìG' estimates for the seed cotton yield, the ìG' estimates were high indicating existence of favourable alleles for further improvement of the target hybrid.

However, to initiate the improvement programme for this cross, further characterization of

Table 5. Estimates of µG' in the donor parents for important quantitative and qualitative traits combined over environments, when the hybrid NDLH 1938 × L 770 (third superior cross) was designated as the hybrid to be improved

Parent	µG'			
	Seed cotton yield plant^{-1} (g)	2.5% Span length (mm)	Lint index (g)	Boll weight (g)
L 788	1.670 [b]	N	N	0.020 [b]
NA 1325	- 7.515 [b]	- 0.855 [a]	N	- 0.115 [b]
L 604	6.140 [b]	N	N	0.067 [b]
SURABHI	0.530 [b]	N	N	0.003 [b]
RAH 1004	8.718 [b]	- 0.155 [a]	N	0.010 [b]
HYPS 152	- 2.842 [b]	- 0.350 [a]	0.192 [a]	0.045 [b]
MCU 5	- 17.275 [a]	0.225 [a]	N	- 0.085 [b]
G COT 16	- 8.455 [a]	0.260 [a]	N	0.300* [a]
SE a	5.337	0.494	0.061	0.087
SE b	5.337	-		0.071
SE c	-	-	-	-
SE d	-	-	-	-

* Larger than 2 x SE; N = µG' values could not obtained

a = q_{j0}, q_{kl} b = q_{j1}, q_{k0} c = q_{j0}, q_{j1} d = q_{k0}, q_{k1}

Standard errors

Class of loci	Case			
	q_{jo} , q_{k1}	q_{j1} , q_{ko}	q_{jo} , q_{j1}	q_{ko} , q_{k1}
µB'	0.112	0.1	-	-
µC'	0.05	0.071	-	-
µD'	0.05	0.071	-	-
µE'	0.132	0.1	-	-
µF'	0.112	0.071	-	-
µG'	0.087	0.071	-	-
µC'+ µF'	0.122	0.1	-	-
µD'+ µE'	0.141	0.122	-	-

a = q_{jo}, q_{kl}; b = q_{ji}, q_{ko}; c= q_{jo}, q_{ji}; d= q_{ko}, q_{kl}

Table 6. Estimates of μB' …… μG' for boll weight in eight donor parents when NDLH 1938 × L 770 is the hybrid to be improved

	Class of loci										
Parents	**μB'**	**μC'**	**μD'**	**μE'**	**μF'**	**μG'**	**μC+F'**	**μD+E'**	**Genetic affinity with**	**Mean *per se* of NDLH 1938 x donor**	**Mean *per se* of L 770 x donor**
L 788	-0.08	0.200*	0.230*	0.02	0.200*	0.02	0.400*	0.250*	L 770	4.28	4.22
NA 1325	-0.18	0.13	0.300*	0.09	0.13	-0.115	0.260*	0.390*	L 770	4.15	3.81
L 604	0.137	0.018	0.412*	0.202*	0.018	0.067	0.035	0.615*	L 770	4.74	3.95
SURABHI	-0.07	0.062	0.367*	0.158	0.062	0.003	0.125	0.525*	L 770	4.52	3.91
RAH 1004	0.17	0.210*	0.220*	0.01	0.210*	0.01	0.420*	0.23	L 770	4.24	4.22
HYPS 152	0.055	0.195*	0.235*	0.025	0.195*	0.045	0.390*	0.260*	L 770	4.34	4.26
MCU 5	-0.15	0.210*	0.220*	0.01	0.210*	-0.085	0.420*	0.230*	L 770	4.05	4.03
G COT 16	-0.04	0.215*	0.215*	-0.27	0.490*	0.300*	0.705*	-0.055	NDLH 1938	4.26	4.81

@ Mean *per se* of the cross NDLH 1938 × L 770 is: 4.64

* Larger than 2 x S.E. a= q_{jo}, q_{k1}; b= q_{j1}, q_{ko}; c= q_{jo}, q_{j1}; d= q_{ko}, q_{k1}

various donor parents and their genetic similarity estimates (Table 6) have to be analyzed critically along with the other estimates (mB' to mG') by considering the genetic enhancement for boll weight. Only one parent out of eight donors i.e., G COT 16 had shown significant positive favourable alleles (ìG'). The parent G COT 16 was found suitable for direct replacement with NDLH 1938.

For enhancing the cross NDLH 1938 × L 770 through parental improvement, G COT 16 and L 604 could also be suggested for L 770 and NDLH 1938 respectively.

CONCLUSION

Identification of unique favourable alleles in the donor parents analysis revealed that for improving NDLH 1938 × RAH 1004 hybrid for 2.5 % span length, the donor parent SURABHI and for lint index donors, L 788 and NA 1325 has shown significant positive ìG' estimates. Whereas, for boll weight three parents, L 788, L 770 and L 604, showed the significant positive ìG' estimates in combined analysis. Only one parent i.e., G COT 16, showed the significant positive ìG' estimates in combined analysis for boll weight for improving NDLH 1938 × L 770 hybrid.

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